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REMARKS

Applicants respectfully request reconsideration of the present application.

1. Disposition of the Claims and Specification

Claims 44-51, 54, and 58-61 are pending. Claims 44, 50 and 51 are currently amended. Claims 61 and 62 are newly added. Support for the amendment to claim 44 may be found in the specification at page 16, line 31 – page 17, line 2. Support for the amendment to claim 51 may be found in the specification at page 17, lines 8-15. Support for claims 61 and 62 may be found in the specification at page 27, lines 17-18. Claim 50 was dependent on a cancelled claim, as a result of a typographical error, and is amended to be dependent on a pending claim.

Because the foregoing amendments do not introduce new matter, entry thereof by the Examiner is respectfully requested.

2. Specification/Information Disclosure Statement

The Examiner indicates that the documents supplied on 1/20/2004 were not considered because they did not comply with 37 C.F.R. § 1.98. Applicants resubmit these documents in the attached information disclosure statement in conformance with 37 C.F.R. 1.98.

3. Claim Rejections – 35 U.S.C. § 101

Claims 44-51, 54, and 58-59 are rejected under 35 U.S.C. § 101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility. The Examiner reasons that “until some actual and specific significance can be attributed to the protein identified in the specification ... the instant invention is incomplete.” Office Action at 3. The Examiner admits that Applicants will satisfy the utility requirement of 35 U.S.C. § 101 by identifying one substantial credible utility, such as an “indicator of a diseased state or of the presence of a disorder.” Office Action at 6. Applicants respectfully request reconsideration and withdrawal of the rejection.

According to the results of the attached BLAST search, performed with SEQ ID NO: 3 of the instant invention, the protein identified in the specification having an amino acid sequence corresponding to SEQ ID NO: 3 is identical to the proteins named p34SEI1 and TRIP-Br1. See BLAST Search Results (Exhibit 1). Sugimoto *et al.*, GENES & DEVELOPMENT 13:3027-3033 (1999), a post-filing date article regarding the p34SEI1 protein, indicates that the p34SEI1 protein antagonizes the function of p16INK4a, which inhibits the cyclin-dependent kinases CDK4 and CDK6. See Sugimoto *et al.*, GENES & DEVELOPMENT 13:3027-3033 (1999). Sugimoto *et al.*, on pages 3031-32, explains that as a modulator of CDK4 kinase activity, p34SEI1 can “contribute to the deregulated growth of tumor cells.” Along these lines, page 27 of the instant specification states that “expression of CECRP is closely associated with cell proliferation.”

Hsu, *et al.*, THE EMBO JOURNAL, Vol. 20, No. 9, pp. 2273-2285 (2001), another post-filing date article, reports that TRIP-Br1 is a transcriptional regulator that stimulates E2F-1/DP-1 transcriptional activity. See Hsu, *et al.*, THE EMBO JOURNAL, Vol. 20, No. 9, pp. 2273-2285 (2001). Hsu, *et al.*, on pages 2282-83, explains that TRIP-Br1 is identical to the cyclin-dependent kinase 4 (cdk4) binding protein p34SEI1, and the BLAST results show that TRIP-Br1 and p34SEI1 are identical to the protein of the instant invention represented by SEQ ID NO: 3.

Accordingly, the claimed proteins and nucleotides of the instant invention do have a determined function with biological significance. Specifically, the claimed protein is related to cell proliferation and CDK4 kinase modulation, as well as transcriptional regulation. Additionally, the claimed protein and nucleotides may be used as a reagent for the diagnosis of a disease involving changes in levels of cyclin-dependent kinases CDK4 and CDK6, or to diagnose a disease implicated by changes in E2F transcriptional activity. Such diseases are disclosed in the specification at page 40. Because the claimed invention has at least one substantial and credible utility, the § 101 rejection is improper and should be withdrawn.

4. Claim Rejections – 35 U.S.C. § 112, First Paragraph

Claims 44-51, 54, and 58-59 are rejected under 35 U.S.C. § 112, first paragraph. Applicants respectfully request reconsideration and withdrawal of the rejection.

The Examiner reasons that because the claimed invention is not supported by either a substantially asserted utility or a well established utility, one skilled in the art clearly would not know how to use the claimed invention. Applicants have established a substantial and well-established utility as described above. The § 112, first paragraph, rejection is improper and should be withdrawn.

Further, the Examiner has rejected claims 44-51, 54, and 58-59 because the instant specification fails to adequately describe and enable proteins that are at least 90% identical to the polypeptide of SEQ ID NO: 3. Applicants do not agree with the Examiner. However, to expedite prosecution, Applicants have amended claims 44 and 51 to avoid this issue. Support for the amendment to claim 44 may be found in the specification at page 16, line 31 – page 17, line 2. Support for the amendment to claim 51 may be found in the specification at page 17, lines 8-15. The present version of the claims avoids this issue. The rejection should be withdrawn.

5. Claim Rejections – 35 U.S.C. § 112, Second Paragraph

Claims 44-51, 54, and 58-59 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Applicants respectfully request reconsideration and withdrawal of the rejection.

The Examiner states that it is unclear what cell cycle regulating activity the claimed protein has. As described above, Applicants have established an actual effect that the claimed protein has on the cell cycle from which one can determine the “metes and bounds of the term ‘cell cycle regulating activity.’” See Office Action at 8. Specifically, Applicants have demonstrated that the claimed protein is associated with unregulated growth of tumor cells, i.e., unregulated cellular proliferation. See Specification page 27, lines 17-18 and Sugimoto

et al., pages 3031-32. Therefore, the § 112, second paragraph, rejection is improper and should be withdrawn.

6. New Claims

Applicants have added new independent claims 61 and 62 to more particularly point out the invention and distinctly claim the subject matter which applicant regards as the invention. New claims 61 and 62 recite a new limitation that the claimed proteins regulate cell proliferation. Support for new claims 61 and 62 may be found at page 27, lines 17-18 of the specification.

Conclusion

Applicants believe that the present application is in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

The Commissioner is hereby authorized to charge any additional fees which may be required regarding this application under 37 C.F.R. §§ 1.16-1.17, or credit any overpayment, to Deposit Account No. 19-0741. Should no proper payment be enclosed herewith, as by a check being in the wrong amount, unsigned, post-dated, otherwise improper or informal or

even entirely missing, the Commissioner is authorized to charge the unpaid amount to Deposit Account No. 19-0741. If any extensions of time are needed for timely acceptance of papers submitted herewith, Applicants hereby petition for such extension under 37 C.F.R. §1.136 and authorizes payment of any such extensions fees to Deposit Account No. 19-0741.

Respectfully submitted,

Date 6/18/04

By Eve L. Frank

FOLEY & LARDNER LLP
Customer Number: 22428
Telephone: (202) 945-6142
Facsimile: (202) 672-5399

Eve L. Frank
Attorney for Applicant
Registration No. 46,785

Enclosure: Results of BLAST Search

SeqServer
biology in silico

BLAST2 Search Results

Sequences

Help

Retrieval

BLAST2

FASTA

ClustalW

CCG Assembly

Phrap

Translation

BLAST2 Manual

Confidential - Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: **blastp**

Sequence ID(s):

☐ 236062CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 236062CD1
(236 letters)

Database: genpept137
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:

Score (bits)	E Value
-----------------	------------

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<input checked="" type="checkbox"/> <u>g21914610</u>	SCDK4-binding protein p34SEI1 [Homo sapiens]	475	e-133
<input checked="" type="checkbox"/> <u>g14029834</u>	TRIP-Br1 [Homo sapiens]	475	e-133
<input checked="" type="checkbox"/> <u>g12803669</u>	CDK4-binding protein p34SEI1 [Homo sapiens]	474	e-132
<input checked="" type="checkbox"/> <u>g6746617</u>	p34SEI-1 [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g16359222</u>	p34SEI-1 [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g14029832</u>	TRIP-Br1 [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g12835034</u>	unnamed protein product [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g12842405</u>	unnamed protein product [Mus musculus]	406	e-112
<input checked="" type="checkbox"/> <u>g14029830</u>	TRIP-Br1 [Mus musculus]	381	e-104

>g6434876 CDK4-binding protein p34SEI1 [Homo sapiens]
Length = 236

Score = 475 bits (1210), Expect = e-133
Identities = 236/236 (100%), Positives = 236/236 (100%)

Query: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPAVASSSLFDLSVLKLHHS LQQS 60

Sbjct: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
Query: 121 DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
Sbjct: 121 DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
Sbjct: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236

>g21914610 SCDK4-binding protein p34SEI1 [Homo sapiens]
Length = 236

Score = 475 bits (1210), Expect = e-133
Identities = 236/236 (100%), Positives = 236/236 (100%)

Query: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
Sbjct: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
Query: 121 DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
Sbjct: 121 DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
Sbjct: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236

>g14029834 TRIP-Brl [Homo sapiens]
Length = 236

Score = 475 bits (1210), Expect = e-133
Identities = 236/236 (100%), Positives = 236/236 (100%)

Query: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
Sbjct: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVAVASSSLFDLSVLKLHHS LQQS 60
Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSADNLLASSDAALSASMASLLE 120
Query: 121 DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
Sbjct: 121 DL SHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
Sbjct: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236

>g12803669 CDK4-binding protein p34SEI1 [Homo sapiens]
Length = 236

Score = 474 bits (1206), Expect = e-132
Identities = 235/236 (99%), Positives = 235/236 (99%)

Query: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHA AVAQAPP AVASSSLFDLSVLKLHHS LQQS 60
ML SKGLKRKREEEEEKEPLAVDSWWLDPGH AVAQAPP AVASSSLFDLSVLKLHHS LQQS
Sbjct: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHTA AVAQAPP AVASSSLFDLSVLKLHHS LQQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE 120
EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS
Sbjct: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR
Sbjct: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236

>g6746617 p34SEI-1 [Mus musculus]
Length = 236

Score = 411 bits (1044), Expect = e-113
Identities = 204/236 (86%), Positives = 214/236 (90%)

Query: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHA AVAQAPP AVASSSLFDLSVLKLHHS LQQS 60
ML SKGLKRKREEEEE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHS L+QS
Sbjct: 1 ML SKGLKRKREEEETMEALSVDSCWLDPSHPAVAQTPPTVASSSLFDLSVVKLHHS LRQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE 120
EPDLRHLVLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVADSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS
Sbjct: 121 DLNHIEDLNQAPQPQADEGPPGRSIGGISPNLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMDVLVGTQALERPPGPGR
Sbjct: 181 MYDSELWLPASEGLKPGPENGPAAKEEPELDEAELDYLMDVLVGTQALERPPGPGR 236

>g16359222 p34SEI-1 [Mus musculus]
Length = 236

Score = 411 bits (1044), Expect = e-113
Identities = 204/236 (86%), Positives = 214/236 (90%)

Query: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHA AVAQAPP AVASSSLFDLSVLKLHHS LQQS 60
ML SKGLKRKREEEEE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHS L+QS
Sbjct: 1 ML SKGLKRKREEEETMEALSVDSCWLDPSHPAVAQTPPTVASSSLFDLSVVKLHHS LRQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE 120
EPDLRHLVLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVADSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS
Sbjct: 121 DLNHIEDLNQAPQPQADEGPPGRSIGGISPNLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMDVLVGTQALERPPGPGR
Sbjct: 181 MYDSELWLPASEGLKPGPENGPAAKEEPELDEAELDYLMDVLVGTQALERPPGPGR 236

>g14029832 TRIP-Brl [Mus musculus]
Length = 236

Score = 411 bits (1044), Expect = e-113
Identities = 204/236 (86%), Positives = 214/236 (90%)

```
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Query: 61  EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE 120
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Sbjct: 61  EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVADSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
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Sbjct: 121 DLNHIEDLNQAPQPQADEGPPGRSIGGISP NLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
          MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMDVLVGTQALERPPGPGR
Sbjct: 181 MYDSELWL PASEGLKPGPENGPAAKEEPELDEAELDYLMDVLVGTQALERPPGPGR 236
```

>g12835034 unnamed protein product [Mus musculus]
Length = 236

Score = 411 bits (1044), Expect = e-113
Identities = 204/236 (86%), Positives = 214/236 (90%)

```
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Sbjct: 1  MLSKGLKRRKEEEEETMEALSVDSCWLDPSHPAVAQTPPTVASSSLFDLSVVKLHHSRQS 60

Query: 61  EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE 120
          EPDLRHLVLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE
Sbjct: 61  EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVADSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
          DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS
Sbjct: 121 DLNHIEDLNQAPQPQADEGPPGRSIGGISP NLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
          MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMDVLVGTQALERPPGPGR
Sbjct: 181 MYDSELWL PASEGLKPGPENGPAAKEEPELDEAELDYLMDVLVGTQALERPPGPGR 236
```

>g12842405 unnamed protein product [Mus musculus]
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Score = 406 bits (1032), Expect = e-112
Identities = 202/236 (85%), Positives = 212/236 (89%)

```
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Sbjct: 1  MLSKGLKRNGEEEEETMEALSVDSCWLDPSHPAVAQTPPTVASSSLFDLSVVKLHHSRQS 60

Query: 61  EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVADNLLASSDAALSASMASLLE 120
          EPDLRHLVLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE
Sbjct: 61  EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVADSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
          DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS
Sbjct: 121 DLNHIEDLNQAPQPQADEGPPGRSIGGISP NLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
```

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLVGTQALERPPGPGR 236
MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMDVLVGTQALERPPGPGR
Sbjct: 181 MYDSELWLPASEGLKPGPENGPAPKEEPELDEAELDYLMDVLVGTQALERPPGPGR 236

>g14029830 TRIP-Brl [Mus musculus]
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Score = 381 bits (968), Expect = e-104
Identities = 190/223 (85%), Positives = 201/223 (89%)

Query: 1 ML SKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPVASSSLFDLSVLKLHHSLOQS 60
ML SKGLKRKRE+EE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHS+QS
Sbjct: 1 ML SKGLKRKREKEETMEALSVDSCWLDPSHPAVAQTPPTVASSSLFDLSVVLHHSRQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPPAAPSVADNLLASSDAALSASMASLLE 120
EPDLRHLVLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVADSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180
DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS
Sbjct: 121 DLNHIEDLNQAPQQADEGPPGRSIGGISPNLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDVLV 223
MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMDVLV
Sbjct: 181 MYDSELWLPASEGLKPGPENGPAPKEEPELDEAELDYLMDVLV 223

Database: genpept137
Posted date: Sep 11, 2003 11:22 AM
Number of letters in database: 474,463,515
Number of sequences in database: 1,534,369

Lambda	K	H
0.310	0.132	0.383

Gapped Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 250279773
Number of Sequences: 1534369
Number of extensions: 11255951
Number of successful extensions: 47209
Number of sequences better than 10.0: 220
Number of HSP's better than 10.0 without gapping: 34
Number of HSP's successfully gapped in prelim test: 192
Number of HSP's that attempted gapping in prelim test: 46850
Number of HSP's gapped (non-prelim): 418
length of query: 236
length of database: 474,463,515
effective HSP length: 59
effective length of query: 177
effective length of database: 383,935,744
effective search space: 67956626688
effective search space used: 67956626688
T: 11
A: 40
X1: 16 (7.2 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 42 (21.7 bits)



Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Books
Search Protein		for				Go	Clear	
Limits		Preview/Index		History		Clipboard		Details
Display	default	Show	20	Send to	File	Get Subsequence		Fe

☐ 1: AAF08349. CDK4-binding prot...[gi:6434876]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAF08349 236 aa linear PRI 02-DEC-1999
 DEFINITION CDK4-binding protein p34SEI1 [Homo sapiens].
 ACCESSION AAF08349
 VERSION AAF08349.1 GI:6434876
 DBSOURCE locus AF117959 accession AF117959.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 236)
 AUTHORS Sugimoto,M., Nakamura,T., Ohtani,N., Hampson,L., Hampson,I.N.,
 Shimamoto,A., Furuichi,Y., Okumura,K., Niwa,S., Taya,Y. and Hara,E.
 TITLE Regulation of CDK4 activity by a novel CDK4-binding protein,
 p34(SEI-1)
 JOURNAL Genes Dev. 13 (22), 3027-3033 (1999)
 MEDLINE 20047903
 PUBMED 10580009
 REFERENCE 2 (residues 1 to 236)
 AUTHORS Hara,E. and Sugimoto,M.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-1999) Cell Cycle Laboratory, Paterson Institute
 for Cancer Research, Wilmslow Road, Manchester M20 4BX, UK
 COMMENT Method: conceptual translation.
 FEATURES
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Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Books
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☐ 1: [AAK52831](#). TRIP-Br1 [Homo sa...[gi:14029834]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAK52831 236 aa linear PRI 13-MAY-2001

DEFINITION TRIP-Br1 [Homo sapiens].

ACCESSION AAK52831

VERSION AAK52831.1 GI:14029834

DBSOURCE locus AF366402 accession [AF366402.1](#)

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 236)

AUTHORS Hsu, S.I., Yang, C.M., Sim, K.G., Hentschel, D.M., O'Leary, E. and Bonventre, J.V.

TITLE TRIP-Br: a novel family of PHD zinc finger- and bromodomain-interacting proteins that regulate the transcriptional activity of E2F-1/DP-1

JOURNAL EMBO J. 20 (9), 2273-2285 (2001)

MEDLINE 21231173

PUBMED 11331592

REFERENCE 2 (residues 1 to 236)

AUTHORS Hsu, S.I. and Bonventre, J.V.

TITLE Direct Submission

JOURNAL Submitted (29-MAR-2001) Dept. of Medicine, National University Hospital, 5 Lower Kent Ridge Road 119074, Singapore

COMMENT Method: conceptual translation.

FEATURES

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